

Sequencing, Finishing, and Analysis in the Future (SFAF)

La Fonda on the Plaza, Santa Fe, NM: May 28th – May 30th, 2014

Call for Abstracts (both talks and posters) Deadline April 11th, 2014

Please join us for the 9th annual "Sequencing, Finishing and Analysis in the Future" Meeting on Wednesday, **May 28th through May 30th** in beautiful, historic Santa Fe, NM. The three day SFAF conference will focus on Next Generation Sequencing technologies, applications, and their effect on the rapidly advancing field of Genomics.

Keynote Speakers:

- Rick Wilson, Ph.D., Director of The Genome Institute at Washington University, and Professor of Genetics
- TBA
- TBA

Areas to be emphasized include, but are not limited to the following:

Genome Sequencing:

- Sequencing strategies and technology advancements using the various NGS platforms
- *De novo* sequencing, re-sequencing, Human seq., RNA seq., metagenomics, etc.
- Sequencing applications for Metagenomics, Forensics, and Biosurveillance



Genome Assembly:

- Whole genome assemblers and integration of next generation data
- *De novo* assemblers for short reads, hybrid assemblers
- Recalling and calibrating genome assemblies
- Single cell and metagenomic assemblies

Genome Finishing / Improvement:

- Next Generation Finishing tools, technologies, and pipelines
- Human Genomics and genome improvement
- Quality standards for new technologies and mixed data sets
- Single cell / cell sorting and metagenomic finishing



Genome Analysis:

- Genome annotation and pathway identification tools and pipelines
- Comparative genomics, re-sequencing, SNPs, structural variation
- Large scale data management, cloud computing
- Analysis applications for Forensics, Metagenomics, and Biosurveillance

Clinical Applications of NGS:

- Bringing sequence to the clinic (i.e. diagnostics)
- Human, non-human, and infectious disease applications

The conference is being sponsored by numerous genomics/sequencing vendors and hosted by the Los Alamos National Laboratory, thus **NO** registration fee is required. Participants need to cover travel costs, hotel and dinner charges. Breakfast, lunch and snacks will be provided. A block of rooms ([SFAF](#)) are reserved at the La Fonda at a special conference rate of \$88 per night. **A limited number of extra rooms are available the weekend before & after the conference for those that want to enjoy the area a little longer (Reserve using [hotel link](#) ASAP).**

Registration is limited to 220; please register soon if you plan to attend. **To register, submit an abstract, or obtain more information as it becomes available please visit our web site, <http://www.lanl.gov/finishinginthefuture/>** **The hotel reservation link can also be found on the SFAF website under the "Eventbrite" link.**

Additionally, we plan to have a job board up at the meeting this year, so please make use of this if you would like to post a job vacancy or if you are looking for something new to try out!

If you have any questions, or would like further information, please contact Chris Detter at (505) 667-1326 or cdetter@lanl.gov or Shannon Johnson at shannonj@lanl.gov

We look forward to seeing you there!!!

The 2014 "Sequencing, Finishing and Analysis in the Future" Organizing Committee:

- * Chris Detter, Ph.D., Senior Science Advisor, DTRA
- * Johar Ali, Ph.D., Cancer Genomics Team Leader, OICR
- * Patrick Chain, Bioinformatics/Metagenomics Team Leader, LANL
- * Michael FitzGerald, Microbial Special Projects Manager, Broad Institute
- * Bob Fulton, M.S., Director of Project Development & Management, WashU
- * Darren Grafham, Lab Manager, Children's Hospital, Sheffield, UK
- * Alla Lapidus, Ph.D., Director, Genomics, Algorithmic Biology Lab, SPbAU; SPbSU, Russia
- * Donna Muzny, M.Sc., Director of Operations, BCM
- * Nadia Fedorova, Genome Finishing and Analysis Team Leader, JCVI
- * David Bruce, Project and Program Manager of Genomic Sciences, LANL
- * Shannon Johnson, Ph.D., Project Manager, LANL
- * Tracy Erkkila, M.S., Technical Project Manager, LANL
- * Tina Graves, M.S., Reference Genomes, WashU